Supplemental Information

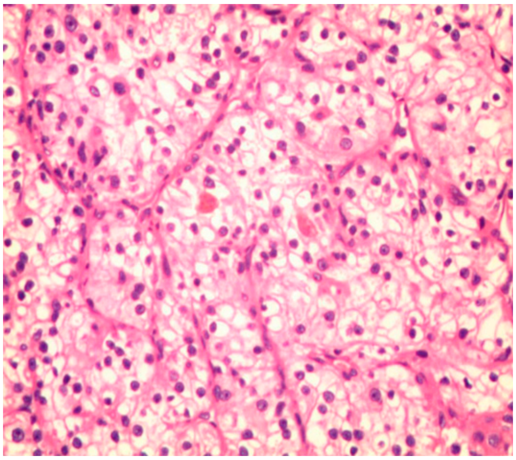

Figure S1. Hematoxylin and Eosin Staining of Clear Cell Renal Cell Tumor from Patient Sampled in This Study, Related to Figure 1

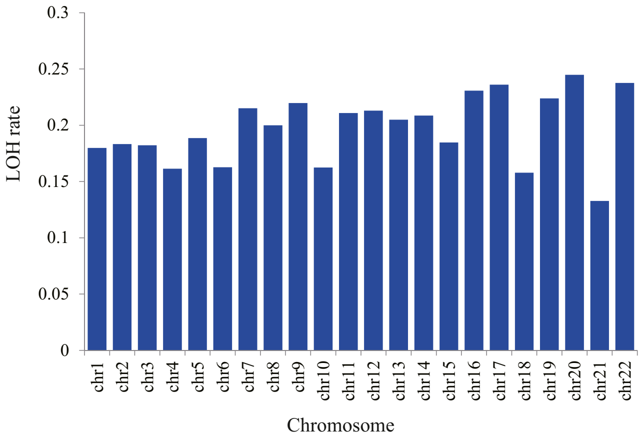

Figure S2. LOH Analysis of Paired Tissue Sequencing Data, Related to Figure 1

The LOH ratio was calculated by N_L/N_H, where N_L is the number of sites that is homozygous sites in cancer tissue and heterozygous in normal tissue, and N_H is the number of sites that are heterozygous in normal tissue.

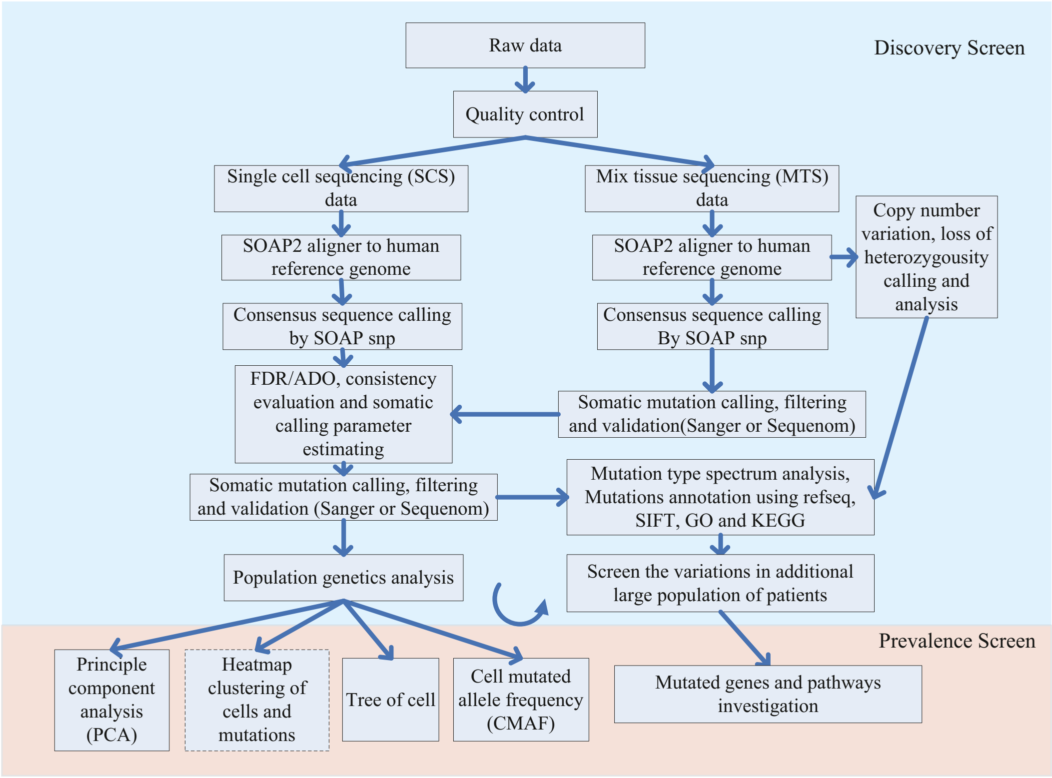

Figure S3. Analysis Pipeline for Single-Cell Sequencing, Related to Figure 2
Dotted rectangles represent analyses that were not performed in this paper.

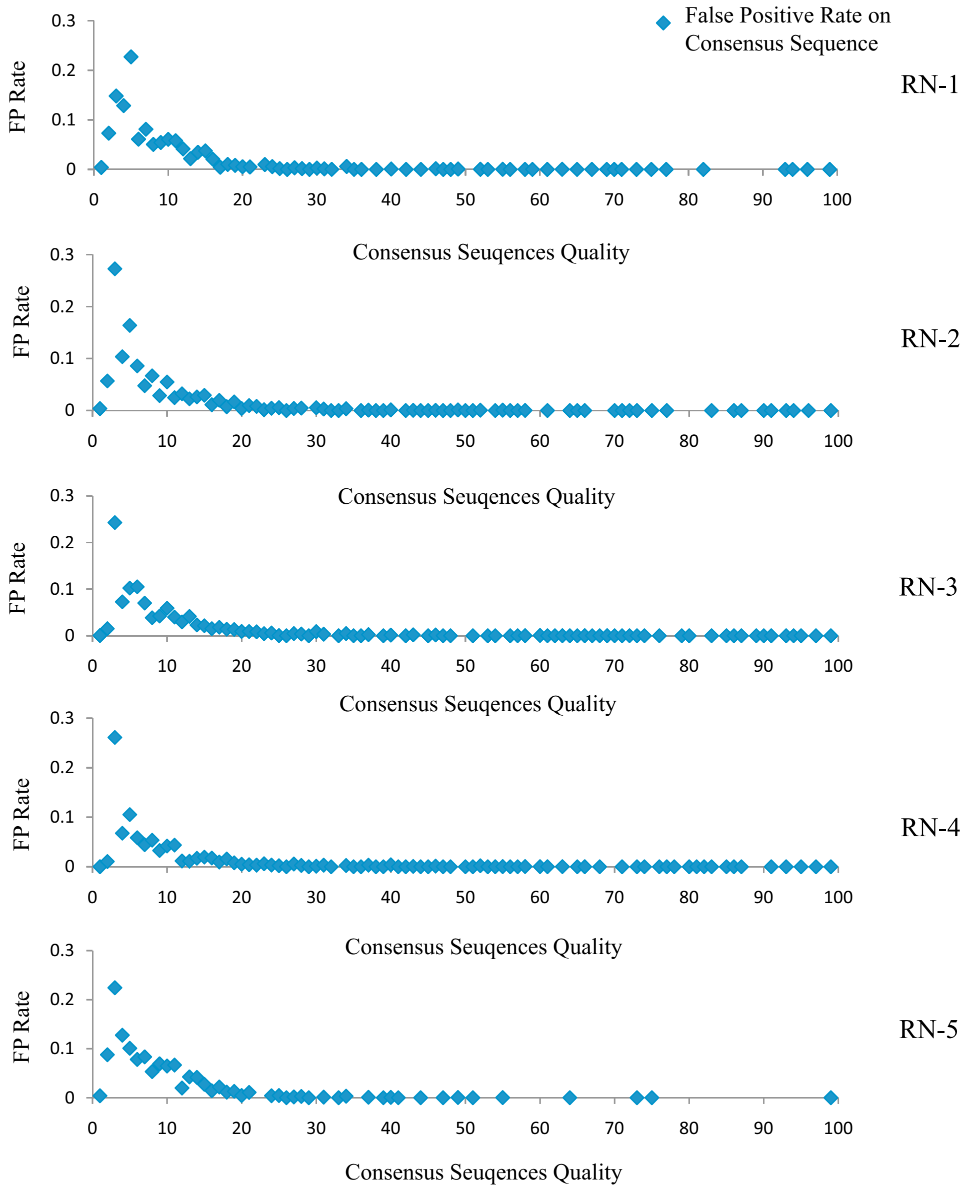

Figure S4. False Positive Rate Distribution across Different Consensus Sequence Quality, Related to Figure 2

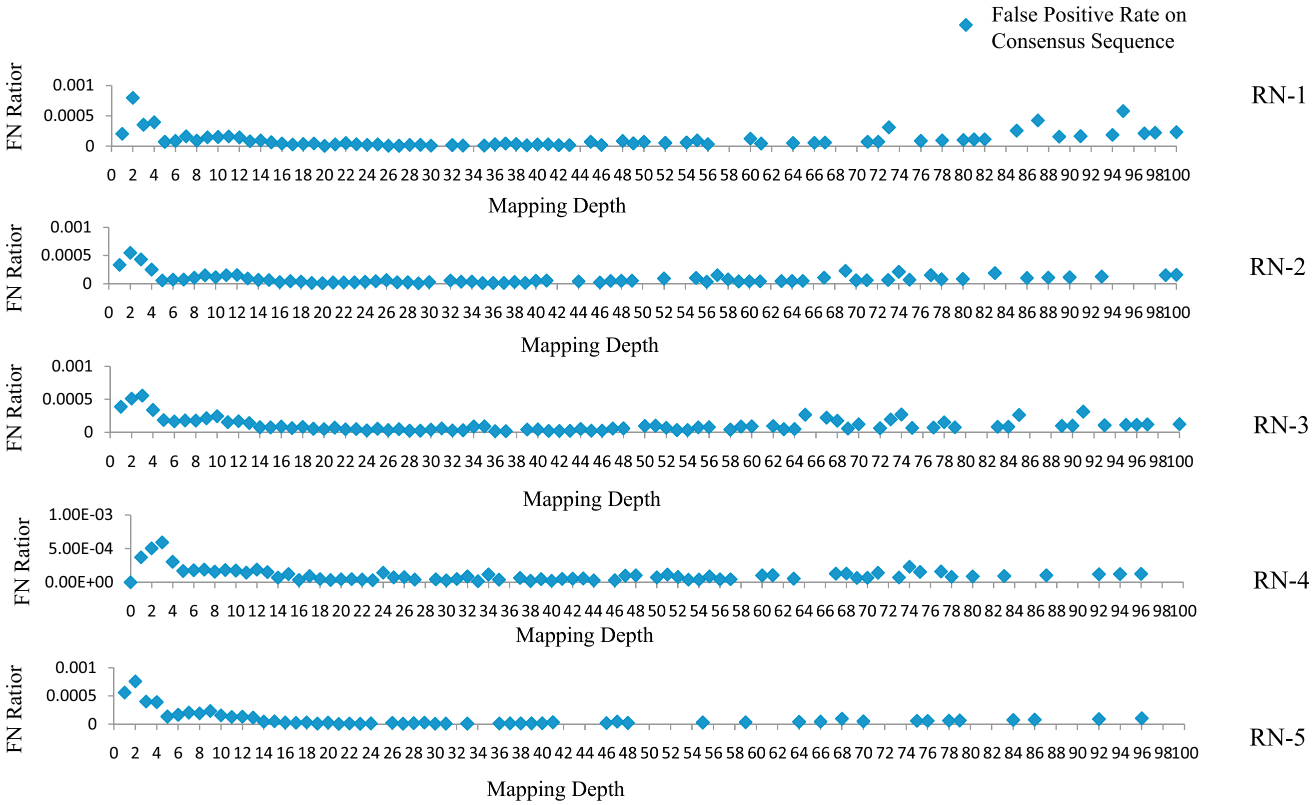

Figure S5. False Positive Rate Distribution across Different Consensus Sequence Depth, Related to Figure 2

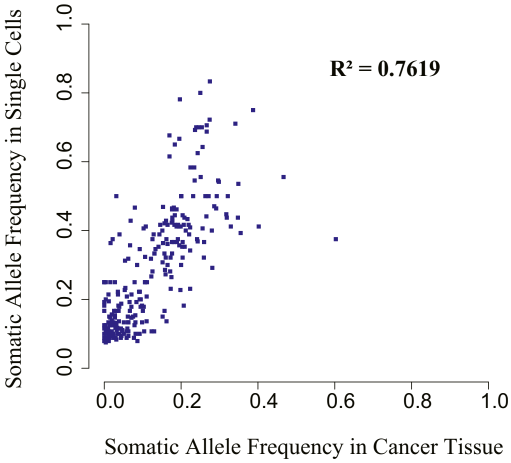

Figure S6. Somatic Mutation Frequency Correlations, Related to Figure 2

Somatic mutation frequency between the single cell data set and the corresponding mixed tissue data (the mutant reads ratio) set estimated using squared correlations of allele frequencies (R^2).